

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Sledziewski Ph.D., Andrzej Z
Bell, Lillian A.
Kindsvogel Ph.D., Wayne R.

(ii) TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
FUSIONS

(iii) NUMBER OF SEQUENCES: 36

(iv) CORRESPONDENCE ADDRESS:

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(B) STREET: 6300 Columbia Center
(C) CITY: Seattle
(D) STATE: WA
(E) COUNTRY: USA
(F) ZIP: 98104-7092

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.24

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/146,877
(B) FILING DATE: 22-JAN-1988

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/347,291
(B) FILING DATE: 02-MAY-1989

(ix) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: 990008.446C3

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7/1020x

00550400 112597

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (D) DEVELOPMENTAL STAGE: Adult
- (F) TISSUE TYPE: Skin
- (G) CELL TYPE: fibroblasts

(vii) IMMEDIATE SOURCE:

- (B) CLONE: pR-rX1

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 354..3671
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCCTCAGCCC TGCTGCCAG CACGAGCCTG TGCTCGCCCT GCCCAACGCA GACAGCCAGA	60
CCCAGGGCGG CCCCTCTGCG GGCTCTGCTC CTCCCGAAGG ATGCTTGGGG AGTGAGGCGA	120
AGCTGGGCGC TCCTCTCCCC TACAGCAGCC CCCTTCCTCC ATCCCTCTGT TCTCCTGAGC	180
CTTCAGGAGC CTGCACCACT CCTGCCTGTC CTTCTACTCA GCTGTTACCC ACTCTGGGAC	240
CAGCAGTCTT TCTGATACT GGGAGAGGGC AGTAAGGAGG ACTTCCTGGA GGGGGTGACT	300
GTCCAGAGCC TGGAACTGTG CCCACACCAG AAGCCATCAG CAGCAAGGAC ACC ATG	356
	Met
	1
CGG CTT CCG GGT GCG ATG CCA GCT CTG GCC CTC AAA GGC GAG CTG CTG	404
Arg Leu Pro Gly Ala Met Pro Ala Leu Ala Leu Lys Gly Glu Leu Leu	
5 10 15	
TTG CTG TCT CTC CTG TTA CTT CTG GAA CCA CAG ATC TCT CAG GGC CTG	452
Leu Leu Ser Leu Leu Leu Leu Glu Pro Gln Ile Ser Gln Gly Leu	
20 25 30	

GTC Val 35	GTC Val 35	ACA Thr	CCC Pro	CCG Pro	GGG Gly	CCA Pro 40	GAG Glu	CTT Leu	GTC Val	CTC Leu	AAT Asn 45	GTC Val	TCC Ser	AGC Ser	ACC Thr	500
TTC Phe 50	GTT Val	CTG Leu	ACC Thr	TGC Cys	TCG Ser 55	GGT Gly	TCA Ser	GCT Ala	CCG Pro	GTG Val 60	GTG Val	TGG Trp	GAA Glu	CGG Arg	ATG Met 65	548
TCC Ser	CAG Gln	GAG Glu	CCC Pro	CCA Pro 70	CAG Gln	GAA Glu	ATG Met	GCC Ala	AAG Lys 75	GCC Ala	CAG Gln	GAT Asp	GGC Gly	ACC Thr 80	TTC Phe	596
TCC Ser	AGC Ser	GTG Val 85	CTC Leu	ACA Thr	CTG Leu	ACC Thr	AAC Asn	CTC Leu 90	ACT Thr	GGG Gly	CTA Leu	GAC Asp	ACG Thr 95	GGA Gly	GAA Glu	644
TAC Tyr	TTT Phe	TGC Cys 100	ACC Thr	CAC His	AAT Asn	GAC Asp 105	TCC Ser	CGT Arg	GGA Gly	CTG Leu	GAG Glu	ACC Thr 110	GAT Asp	GAG Glu	CGG Arg	692
AAA Lys 115	CGG Arg	CTC Leu	TAC Tyr	ATC Ile	TTT Phe	GTG Val 120	CCA Pro	GAT Asp	CCC Pro	ACC Thr 125	GTG Val	GGC Gly	TTC Phe	CTC Leu	CCT Pro	740
AAT Asn 130	GAT Asp	GCC Ala	GAG Glu	GAA Glu	CTA Phe 135	TTC Phe	ATC Ile	TTT Phe	CTC Leu	ACG Thr 140	GAA Glu	ATA Ile	ACT Thr	GAG Glu	ATC Ile 145	788
ACC Thr	ATT Ile	CCA Pro	TGC Cys	CGA Arg 150	GTA Val	ACA Thr	GAC Asp	CCA Pro	CAG Gln 155	CTG Leu	GTG Val	GTG Val	ACA Thr	CTG Leu	CAC His 160	836
GAG Glu	AAG Lys	AAA Lys	GGG Gly 165	GAC Asp	GTT Val	GCA Ala	CTG Leu	CCT Pro 170	GTC Val	CCC Pro	TAT Tyr	GAT Asp	CAC His 175	CAA Gln	CGT Arg	884
GGC Gly	TTT Phe	TCT Ser 180	GGT Gly	ATC Ile	TTT Phe	GAG Glu 185	GAC Asp	AGA Arg	AGC Ser	TAC Tyr	ATC Ile	TGC Cys 190	AAA Lys	ACC Thr	ACC Thr	932
ATT Ile 195	GGG Gly	GAC Asp	AGG Arg	GAG Glu	GTG Val 200	GAT Asp	TCT Ser	GAT Asp	GCC Ala	TAC Tyr 205	TAT Tyr	GTC Val	TAC Tyr	AGA Arg	CTC Leu	980
CAG Gln 210	GTG Val	TCA Ser	TCC Ser	ATC Ile	AAC Asn 215	GTC Val	TCT Ser	GTG Val	AAC Asn	GCA Ala 220	GTG Val	CAG Gln	ACT Thr	GTG Val	GTC Val 225	1028
CGC Arg	CAG Gln	GGT Gly	GAG Glu	AAC Asn 230	ATC Ile	ACC Thr	CTC Leu	ATG Met	TGC Cys 235	ATT Ile	GTG Val	ATC Ile	GGG Gly	AAT Asn 240	GAG Glu	1076
GTG Val	GTC Val	AAC Asn 245	TTC Phe	GAG Glu	TGG Trp	ACA Thr	TAC Tyr	CCC Pro 250	CGC Arg	AAA Lys	GAA Glu	AGT Ser	GGG Gly	CGG Arg	CTG Leu	1124

GTG Val	GAG Glu	CCG Pro	GTG Val	ACT Thr	GAC Asp	TTC Phe	CTC Leu	TTG Leu	GAT Asp	ATG Met	CCT Pro	TAC Tyr	CAC His	ATC Ile	CGC Arg	1172
260																
TCC Ser	ATC Ile	CTG Leu	CAC His	ATC Ile	CCC Pro	AGT Ser	GCC Ala	GAG Glu	TTA Leu	GAA Glu	GAC Asp	TCG Ser	GGG Gly	ACC Thr	TAC Tyr	1220
275																
ACC Thr	TGC Cys	AAT Asn	GTG Val	ACG Thr	GAG Glu	AGT Ser	GTG Val	AAT Asn	GAC Asp	CAT His	CAG Gln	GAT Asp	GAA Glu	AAG Lys	GCC Ala	1268
290																
ATC Ile	AAC Asn	ATC Ile	ACC Thr	GTG Val	GTT Val	GAG Glu	AGC Ser	GGC Gly	TAC Tyr	GTG Val	CGG Arg	CTC Leu	CTG Leu	GGA Gly	GAG Glu	1316
310																
GTG Val	GGC Gly	ACA Thr	CTA Leu	CAA Gln	TTT Phe	GCT Ala	GAG Glu	CTG Leu	CAT His	CGG Arg	AGC Ser	CGG Arg	ACA Thr	CTG Leu	CAG Gln	1364
325																
GTA Val	GTG Val	TTC Phe	GAG Glu	GCC Ala	TAC Tyr	CCA Pro	CCG Pro	CCC Pro	ACT Thr	GTC Val	CTG Leu	TGG Trp	TTC Phe	AAA Lys	GAC Asp	1412
340																
AAC Asn	CGC Arg	ACC Thr	CTG Leu	GGC Gly	GAC Asp	TCC Ser	AGC Ser	GCT Ala	GGC Gly	GAA Glu	ATC Ile	GCC Ala	CTG Leu	TCC Ser	ACG Thr	1460
355																
CGC Arg	AAC Asn	GTG Val	TCG Ser	GAG Glu	ACC Thr	CGG Arg	TAT Tyr	GTG Val	TCA Ser	GAG Glu	CTG Leu	ACA Thr	CTG Leu	GTT Val	CGC Arg	1508
370																
GTG Val	AAG Lys	GTG Val	GCA Ala	GAG Glu	GCT Ala	GGC Gly	CAC His	TAC Tyr	ACC Thr	ATG Met	CGG Arg	GCC Ala	TTC Phe	CAT His	GAG Glu	1556
390																
GAT Asp	GCT Ala	GAG Glu	GTC Val	CAG Gln	CTC Leu	TCC Ser	TTC Phe	CAG Gln	CTA Leu	CAG Gln	ATC Ile	AAT Asn	GTC Val	CCT Pro	GTC Val	1604
405																
CGA Arg	GTG Val	CTG Leu	GAG Glu	CTA Leu	AGT Ser	GAG Glu	AGC Ser	CAC His	CCT Pro	GAC Asp	AGT Ser	GGG Gly	GAA Glu	CAG Gln	ACA Thr	1652
420																
GTC Val	CGC Arg	TGT Cys	CGT Arg	GGC Gly	CGG Arg	GGC Gly	ATG Met	CCC Pro	CAG Gln	CCG Pro	AAC Asn	ATC Ile	ATC Ile	TGG Trp	TCT Ser	1700
435																
GCC Ala	TGC Cys	AGA Arg	GAC Asp	CTC Leu	AAA Lys	AGG Arg	TGT Cys	CCA Pro	CGT Arg	GAG Glu	CTG Leu	CCG Pro	CCC Pro	ACG Thr	CTG Leu	1748
450																
455																
460																
465																

CTG GGG AAC AGT TCC GAA GAG GAG AGC CAG CTG GAG ACT AAC GTG ACG Leu Gly Asn Ser Ser Glu Glu Glu Ser Gln Leu Glu Thr Asn Val Thr 470 475 480	1796
TAC TGG GAG GAG GAG CAG GAG TTT GAG GTG GTG AGC ACA CTG CGT CTG Tyr Trp Glu Glu Glu Gln Glu Phe Glu Val Val Ser Thr Leu Arg Leu 485 490 495	1844
CAG CAC GTG GAT CGG CCA CTG TCG GTG CGC TGC ACG CTG CGC AAC GCT Gln His Val Asp Arg Pro Leu Ser Val Arg Cys Thr Leu Arg Asn Ala 500 505 510	1892
GTG GGC CAG GAC ACG CAG GAG GTC ATC GTG GTG CCA CAC TCC TTG CCC Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser Leu Pro 515 520 525	1940
TTF AAG GTG GTG GTG ATC TCA GCC ATC CTG GCC CTG GTG GTG CTC ACC Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu Thr 530 535 540 545	1988
ATC ATC TCC CTT ATC ATC CTC ATC ATG CTT TGG CAG AAG AAG CCA CGT Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro Arg 550 555 560	2036
TAC GAG ATC CGA TGG AAG GTG ATT GAG TCT GTG AGC TCT GAC GGC CAT Tyr Glu Ile Arg Trp Lys Val Ile Glu Ser Val Ser Ser Asp Gly His 565 570 575	2084
GAG TAC ATC TAC GTG GAC CCC ATG CAG CTG CCC TAT GAC TCC ACG TGG Glu Tyr Ile Tyr Val Asp Pro Met Gln Leu Pro Tyr Asp Ser Thr Trp 580 585 590	2132
GAG CTG CCG CGG GAC CAG CTT GTG CTG GGA CGC ACC CTC GGC TCT GGG Glu Leu Pro Arg Asp Gln Leu Val Leu Gly Arg Thr Leu Gly Ser Gly 595 600 605	2180
GCC TTT GGG CAG GTG GTG GAG GCC ACG GCT CAT GGC CTG AGC CAT TCT Ala Phe Gly Gln Val Val Glu Ala Thr Ala His Gly Leu Ser His Ser 610 615 620 625	2228
CAG GCC ACG ATG AAA GTG GCC GTC AAG ATG CTT AAA TCC ACA GCC CGC Gln Ala Thr Met Lys Val Ala Val Lys Met Leu Lys Ser Thr Ala Arg 630 635 640	2276
AGC AGT GAG AAG CAA GCC CTT ATG TCG GAG CTG AAG ATC ATG AGT CAC Ser Ser Glu Lys Gln Ala Leu Met Ser Glu Leu Lys Ile Met Ser His 645 650 655	2324
CTT GGG CCC CAC CTG AAC GTG GTC AAC CTG TTG GGG GCC TGC ACC AAA Leu Gly Pro His Leu Asn Val Val Asn Leu Leu Gly Ala Cys Thr Lys 660 665 670	2372
GGA GGA CCC ATC TAT ATC ATC ACT GAG TAC TGC CGC TAC GGA GAC CTG Gly Gly Pro Ile Tyr Ile Ile Thr Glu Tyr Cys Arg Tyr Gly Asp Leu 675 680 685	2420

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ACC TTG GGT GGC ACC CCT TAC CCA GAG CTG CCC ATG AAC GAG CAG TTC Thr Leu Gly Gly Thr Pro Tyr Pro Glu Leu Pro Met Asn Glu Gln Phe 900 905 910	3092
TAC AAT GCC ATC AAA CGG GGT TAC CGC ATG GCC CAG CCT GCC CAT GCC Tyr Asn Ala Ile Lys Arg Gly Tyr Arg Met Ala Gln Pro Ala His Ala 915 920 925	3140
TCC GAC GAG ATC TAT GAG ATC ATG CAG AAG TGC TGG GAA GAG AAG TTT Ser Asp Glu Ile Tyr Glu Ile Met Gln Lys Cys Trp Glu Glu Lys Phe 930 935 940 945	3188
GAG ATT CGG CCC CCC TTC TCC CAG CTG GTG CTG CTT CTC GAG AGA CTG Glu Ile Arg Pro Pro Phe Ser Gln Leu Val Leu Leu Leu Glu Arg Leu 950 955 960	3236
TTG GGC GAA GGT TAC AAA AAG AAG TAC CAG CAG GTG GAT GAG GAG TTT Leu Gly Glu Gly Tyr Lys Lys Lys Tyr Gln Gln Val Asp Glu Glu Phe 965 970 975	3284
CTG AGG AGT GAC CAC CCA GCC ATC CTT CGG TCC CAG GCC CGC TTG CCT Leu Arg Ser Asp His Pro Ala Ile Leu Arg Ser Gln Ala Arg Leu Pro 980 985 990	3332
GGG TTC CAT GGC CTC CGA TCT CCC CTG GAC ACC AGC TCC GTC CTC TAT Gly Phe His Gly Leu Arg Ser Pro Leu Asp Thr Ser Ser Val Leu Tyr 995 1000 1005	3380
ACT GCC GTG CAG CCC AAT GAG GGT GAC AAC GAC TAT ATC ATC CCC CTG Thr Ala Val Gln Pro Asn Glu Gly Asp Asn Asp Tyr Ile Ile Pro Leu 1010 1015 1020 1025	3428
CCT GAC CCC AAA CCC GAG GTT GCT GAC GAG GGC CCA CTG GAG GGT TCC Pro Asp Pro Lys Pro Glu Val Ala Asp Glu Gly Pro Leu Glu Gly Ser 1030 1035 1040	3476
CCC AGC CTA GCC AGC TCC ACC CTG AAT GAA GTC AAC ACC TCC TCA ACC Pro Ser Leu Ala Ser Ser Thr Leu Asn Glu Val Asn Thr Ser Ser Thr 1045 1050 1055	3524
ATC TCC TGT GAC AGC CCC CTG GAG CCC CAG GAC GAA CCA GAG CCA GAG Ile Ser Cys Asp Ser Pro Leu Glu Pro Gln Asp Glu Pro Glu Pro Glu 1060 1065 1070	3572
CCC CAG CTT GAG CTC CAG GTG GAG CCG GAG CCA GAG CTG GAA CAG TTG Pro Gln Leu Glu Leu Gln Val Glu Pro Glu Pro Glu Leu Gln Leu 1075 1080 1085	3620
CCG GAT TCG GGG TGC CCT GCG CCT CGG GCG GAA GCA GAG GAT AGC TTC Pro Asp Ser Gly Cys Pro Ala Pro Arg Ala Glu Ala Glu Asp Ser Phe 1090 1095 1100 1105	3668
CTG TAGGGGGCTG GCCCCTACCC TGCCCTGCCT GAAGCTCCCC CCCTGCCAGC Leu	3721

ACCCAGCATC TCCTGGCCTG GCCTGACCGG GCTTCCTGTC AGCCAGGCTG CCCTTATCAG 3781
 CTGTCCCTT CTGGAAGCTT TCTGCTCCTG ACGTGTGTG CCCCAAACCC TGGGGCTGGC 3841
 TTAGGAGGCA AGAAACTGC AGGGGCCGTG ACCAGCCCTC TGCCTCCAGG GAGGCCAACT 3901
 GACTCTGAGC CAGGGTTCCC CCAGGGAAC TCAATTTCCC ATATGTAAGA TGGGAAAGTT 3961
 AGGCTTGATG ACCCAGAATC TAGGATTCTC TCCCTGGCTG ACACGGTGGG GAGACCGAAT 4021
 CCCTCCCTGG GAAGATTCTT GGAGTTACTG AGGTGGTAAA TTAACATTTT TTCTGTTGAG 4081
 CCAGCTACCC CTCAAGGAAT CATAGCTCTC TCCTCGCACT TTTTATCCAC CCAGGAGCTA 4141
 GGGGAAGAGAC CCTAGCCTCC CTGGCTGCTG GCTGAGCTAG GGCCTAGCTT GAGCAGTGT 4201
 GCCTCATCCA GAAGAAAGCC AGTCTCCTCC CTATGATGCC AGTCCCTGCG TTCCCTGGCC 4261
 CGAGCTGGTC TGGGGCCATT AGGCAGCCTA ATTAATGCTG GAGGCTGAGC CAAGTACAGG 4321
 ACACCCCCAG CCTGCAGCCC TTGCCAGGG CACTTGGAGC ACACGCAGCC ATAGCAAGTG 4381
 CCTGTGTCCC TGTCTTCAG GCCCATCAGT CCTGGGGCTT TTTCTTATC ACCCTCAGT 4441
 TTAATCCATC CACCAGAGTC TAGA 4465

(2) INFORMATION FOR SEQ ID NO:2:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Leu Pro Gly Ala Met Pro Ala Leu Ala Leu Lys Gly Glu Leu
 1 5 10 15
 Leu Leu Leu Ser Leu Leu Leu Leu Glu Pro Gln Ile Ser Gln Gly
 20 25 30
 Leu Val Val Thr Pro Pro Gly Pro Glu Leu Val Leu Asn Val Ser Ser
 35 40 45
 Thr Phe Val Leu Thr Cys Ser Gly Ser Ala Pro Val Val Trp Glu Arg
 50 55 60
 Met Ser Gln Glu Pro Pro Gln Glu Met Ala Lys Ala Gln Asp Gly Thr
 65 70 75 80

Phe Ser Ser Val Leu Thr Leu Thr Asn Leu Thr Gly Leu Asp Thr Gly
 85 90 95
 Glu Tyr Phe Cys Thr His Asn Asp Ser Arg Gly Leu Glu Thr Asp Glu
 100 105 110
 Arg Lys Arg Leu Tyr Ile Phe Val Pro Asp Pro Thr Val Gly Phe Leu
 115 120 125
 Pro Asn Asp Ala Glu Glu Leu Phe Ile Phe Leu Thr Glu Ile Thr Glu
 130 135 140
 Ile Thr Ile Pro Cys Arg Val Thr Asp Pro Gln Leu Val Val Thr Leu
 145 150 155 160
 His Glu Lys Lys Gly Asp Val Ala Leu Pro Val Pro Tyr Asp His Gln
 165 170 175
 Arg Gly Phe Ser Gly Ile Phe Glu Asp Arg Ser Tyr Ile Cys Lys Thr
 180 185 190
 Thr Ile Gly Asp Arg Glu Val Asp Ser Asp Ala Tyr Tyr Val Tyr Arg
 195 200 205
 Leu Gln Val Ser Ser Ile Asn Val Ser Val Asn Ala Val Gln Thr Val
 210 215 220
 Val Arg Gln Gly Glu Asn Ile Thr Leu Met Cys Ile Val Ile Gly Asn
 225 230 235 240
 Glu Val Val Asn Phe Glu Trp Thr Tyr Pro Arg Lys Glu Ser Gly Arg
 245 250 255
 Leu Val Glu Pro Val Thr Asp Phe Leu Leu Asp Met Pro Tyr His Ile
 260 265 270
 Arg Ser Ile Leu His Ile Pro Ser Ala Glu Leu Glu Asp Ser Gly Thr
 275 280 285
 Tyr Thr Cys Asn Val Thr Glu Ser Val Asn Asp His Gln Asp Glu Lys
 290 295 300
 Ala Ile Asn Ile Thr Val Val Glu Ser Gly Tyr Val Arg Leu Leu Gly
 305 310 315 320
 Glu Val Gly Thr Leu Gln Phe Ala Glu Leu His Arg Ser Arg Thr Leu
 325 330 335
 Gln Val Val Phe Glu Ala Tyr Pro Pro Pro Thr Val Leu Trp Phe Lys
 340 345 350
 Asp Asn Arg Thr Leu Gly Asp Ser Ser Ala Gly Glu Ile Ala Leu Ser
 355 360 365

08980400 112597

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His Leu Gly Pro His Leu Asn Val Val Asn Leu Leu Gly Ala Cys Thr
 660 665 670
 Lys Gly Gly Pro Ile Tyr Ile Ile Thr Glu Tyr Cys Arg Tyr Gly Asp
 675 680 685
 Leu Val Asp Tyr Leu His Arg Asn Lys His Thr Phe Leu Gln His His
 690 695 700
 Ser Asp Lys Arg Arg Pro Pro Ser Ala Glu Leu Tyr Ser Asn Ala Leu
 705 710 715 720
 Pro Val Gly Leu Pro Leu Pro Ser His Val Ser Leu Thr Gly Glu Ser
 725 730 735
 Asp Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Val Asp Tyr Val
 740 745 750
 Pro Met Leu Asp Met Lys Gly Asp Val Lys Tyr Ala Asp Ile Glu Ser
 755 760 765
 Ser Asn Tyr Met Ala Pro Tyr Asp Asn Tyr Val Pro Ser Ala Pro Glu
 770 775 780
 Arg Thr Cys Arg Ala Thr Leu Ile Asn Glu Ser Pro Val Leu Ser Tyr
 785 790 795 800
 Met Asp Leu Val Gly Phe Ser Tyr Gln Val Ala Asn Gly Met Glu Phe
 805 810 815
 Leu Ala Ser Lys Asn Cys Val His Arg Asp Leu Ala Ala Arg Asn Val
 820 825 830
 Leu Ile Cys Glu Gly Lys Leu Val Lys Ile Cys Asp Phe Gly Leu Ala
 835 840 845
 Arg Asp Ile Met Arg Asp Ser Asn Tyr Ile Ser Lys Gly Ser Thr Phe
 850 855 860
 Leu Pro Leu Lys Trp Met Ala Pro Glu Ser Ile Phe Asn Ser Leu Tyr
 865 870 875 880
 Thr Thr Leu Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile
 885 890 895
 Phe Thr Leu Gly Gly Thr Pro Tyr Pro Glu Leu Pro Met Asn Glu Gln
 900 905 910
 Phe Tyr Asn Ala Ile Lys Arg Gly Tyr Arg Met Ala Gln Pro Ala His
 915 920 925
 Ala Ser Asp Glu Ile Tyr Glu Ile Met Gln Lys Cys Trp Glu Glu Lys
 930 935 940

Phe Glu Ile Arg Pro Pro Phe Ser Gln Leu Val Leu Leu Leu Glu Arg
 945 950 955 960
 Leu Leu Gly Glu Gly Tyr Lys Lys Lys Tyr Gln Gln Val Asp Glu Glu
 965 970 975
 Phe Leu Arg Ser Asp His Pro Ala Ile Leu Arg Ser Gln Ala Arg Leu
 980 985 990
 Pro Gly Phe His Gly Leu Arg Ser Pro Leu Asp Thr Ser Ser Val Leu
 995 1000 1005
 Tyr Thr Ala Val Gln Pro Asn Glu Gly Asp Asn Asp Tyr Ile Ile Pro
 1010 1015 1020
 Leu Pro Asp Pro Lys Pro Glu Val Ala Asp Glu Gly Pro Leu Glu Gly
 1025 1030 1035 1040
 Ser Pro Ser Leu Ala Ser Ser Thr Leu Asn Glu Val Asn Thr Ser Ser
 1045 1050 1055
 Thr Ile Ser Cys Asp Ser Pro Leu Glu Pro Gln Asp Glu Pro Glu Pro
 1060 1065 1070
 Glu Pro Gln Leu Glu Leu Gln Val Glu Pro Glu Pro Glu Leu Glu Gln
 1075 1080 1085
 Leu Pro Asp Ser Gly Cys Pro Ala Pro Arg Ala Glu Ala Glu Asp Ser
 1090 1095 1100
 Phe Leu
 1105

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
 (B) CLONE: ZC871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATTATACGCT CTCTCCTCA GGTAATGAG TGCCAGGGCC GGCAAGCCCC CGCTCCA

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
 (B) CLONE: ZC872

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCGGGGGAGCG GGGGCTTGCC GGCCCTGGCA CTCATTTACC TGAGGAAGAG AGAGCT

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(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
 (B) CLONE: ZC904

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CATGGGCACG TAATCTATAG ATTATCCTT GCTCATATCC ATGTA

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(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Other nucleic acid
- (iii) HYPOTHETICAL: N
- (iv) ANTI-SENSE: N
- (vii) IMMEDIATE SOURCE:
(B) CLONE: ZC906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGCTGTCCT CTGCTTCAGC CAGAGGTCCT GGGCAGCC

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(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Other nucleic acid
- (iii) HYPOTHETICAL: N
- (iv) ANTI-SENSE: N
- (vii) IMMEDIATE SOURCE:
(B) CLONE: ZC906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGCTGTCCT CTGCTTCAGC CAGAGGTCCT GGGCAGCC

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(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Other nucleic acid
- (iii) HYPOTHETICAL: N
- (iv) ANTI-SENSE: N
- (vii) IMMEDIATE SOURCE:
(B) CLONE: ZC1380

159277 00408690

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATGGTGGAA TTCCTGCTGA T

21

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

—(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: ZC1447

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGGTTGTGCA GAGCTGAGGA AGAGATGGA

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(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: ZC1453

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AATTCATTAT GTTGTGCAA GCCTTCTTGT TCCTGCTAGC TGGTTTCGCT GTTAA

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(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: ZC1454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GATCTTAACA GCGAAACCAG CTAGCAGGAA CAAGAAGGCT TGCAACAACA TAATG

55

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: ZC1478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATCGCGAGCA TGCAGATCTG A

21

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC1479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCTTCAGAT CTGCATGCTG CCGAT

25

(2) INFORMATION FOR SEQ ID NO:14:

— (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC1776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGCTGAGCGC AAATGTTGTG TCGAGTGCCC ACCGTGCCCA GCTTAGAATT CT

52

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC1777

00403500

118

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTAGAGAATT CTAAGCTGGG CACGGTGGGC ACTCGACACA ACATTGCGC TC

52

(2) INFORMATION FOR SEQ ID NO:16:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
 (B) CLONE: ZC1846

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATCGGCCAC TGTCGGTGCG CTGCACGCTG CGCAACGCTG TGGGCCAGGA CACGCAGGAG

60

GTCATCGTGG TGCCCACTC CTTGCCCTTT AAGCA

95

(2) INFORMATION FOR SEQ ID NO:17:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
 (B) CLONE: ZC1847

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGCTTGCTTA AAGGGCAAGG AGTGTGGCAC CACGATGACC TCCTGCGTGT CCTGGCCCCAC

60

AGCGTTGCGC AGCGTGCAGC GCACCGACAG TGGCC

95

119

08980400.12697

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: ZC1886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCAGTGCCAA GCTTGCTAG ACTTACCTTT AAAGGGCAAG GAG

43

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: ZC1892

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCTTGAGCG T

11

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

120

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC1893

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CTAGACGCTC A

11

(2) INFORMATION FOR SEQ ID NO:21:

— (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC1894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGCTTCAGT TCTTCGGCCT CATGTCAGTT CTCGGCCTC ATGTGAT

47

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC1895

121

00980400-112697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTAGATCACA TGAGGCCGAA GAACTGACAT GAGGCCGAAG AACTGGA

47

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZC2181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AATTCGGATC CACCATGGGC ACCAGCCACC CGGCGTTCCT GGTGTTAGGC TGCCTGCTGA
CCGGCC

60

66

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZC2182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGAGCCTGAT CCTGTGCCAA CTGAGCCTGC CATCGATCCT GCCAAACGAG AACGAGAAGG
TTGTGCAGCT A

60

71

00900400 112697

122

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
 (B) CLONE: ZC2183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AATTAGCTG CACAACCTTC TCGTTCTCGT TTGGCAGGAT CGATGGCAGG CTCAGTTGGC 60
 ACAGGATCA 69

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
 (B) CLONE: ZC2184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGCTCAGGCC GGTCAGCAGG CAGCCTAACA CCAGGAACGC CGGGTGGCTG GTGCCCATGG 60
 TGGATCCG 68

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid

123

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC2311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGATCACCAT GGCTCAACTG

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC2351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CGAATTCAC

10

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

124

00500400 112697

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC2352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATTATACGCA TGGTGGAATT CGAGCT

26

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC2392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ACGTAAGCTT GTCTAGACTT ACCTTCAGAA CGCAGGGTGG G

41

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: C-terminal

(vii) IMMEDIATE SOURCE:
(B) CLONE: pWK1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Ala Leu His Asn His Tyr Thr Glu Lys Ser Leu Ser Leu Ser Pro Gly
1 5 10 15

Lys

00990400 112697

125

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

—(x1) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGTGACACTC TCCTGGGAGT TA

22

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GCATAGTAGT TACCATATCC TCTTGCACAG

30

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

00530400 112657

1260

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ACCGAACGTG AGAGGAGTGC TATAA

25

(2) INFORMATION FOR SEQ ID NO:35:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4054 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(111) HYPOTHETICAL: N

(1v) ANTI-SENSE: N

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: p-alpha-17B

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 205..3471
- (D) OTHER INFORMATION:

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCCCTGGGGA CGGACCGTGG GCGGCGCGCA GCGGCGGGAC GCGTTTTGGG GACGTGGTGG	60
CCAGCGCCTT CCTGCAGACC CACAGGGAAG TACTCCCTTT GACCTCCGGG GAGCTGCGAC	120
CAGGTTATAC GTTGCTGGTG GAAAAGTGAC AATTCTAGGA AAAGAGCTAA AAGCCGGATC	180
GGTGACCGAA AGTTTCCCAG AGCT ATG GGG ACT TCC CAT CCG GCG TTC CTG	231
Met Gly Thr Ser His Pro Ala Phe Leu	
1 5	
GTC TTA GGC TGT CTT CTC ACA GGG CTG AGC CTA ATC CTC TGC CAG CTT	279
Val Leu Gly Cys Leu Leu Thr Gly Leu Ser Leu Ile Leu Cys Gln Leu	
10 15 20 25	
TCA TTA CCC TCT ATC CTT CCA AAT GAA AAT GAA AAG GTT GTG CAG CTG	327
Ser Leu Pro Ser Ile Leu Pro Asn Glu Asn Glu Lys Val Val Gln Leu	
30 35 40	
AAT TCA TCC TTT TCT CTG AGA TGC TTT GGG GAG AGT GAA GTG AGC TGG	375
Asn Ser Ser Phe Ser Leu Arg Cys Phe Gly Glu Ser Glu Val Ser Trp	
45 50 55	

08530400 112697

127

CAG Gln	TAC Tyr	CCC Pro	ATG Met	TCT Ser	GAA Glu	GAA Glu	GAG Glu	AGC Ser	TCC Ser	GAT Asp	GTG Val	GAA Glu	ATC Ile	AGA Arg	AAT Asn	423
		60					65					70				
GAA Glu	GAA Glu	AAC Asn	AAC Asn	AGC Ser	GGC Gly	CTT Leu	TTT Phe	GTG Val	ACG Thr	GTC Val	TTG Leu	GAA Glu	GTG Val	AGC Ser	AGT Ser	471
	75					80					85					
GCC Ala	TCG Ser	GCG Ala	GCC Ala	CAC His	ACA Gly	GGG Leu	TTG Tyr	TAC Thr	ACT Cys	TGC Tyr	TAT Tyr	TAC Tyr	AAC Asn	CAC His	ACT Thr	519
	90				95				100						105	
CAG Gln	ACA Thr	GAA Glu	GAG Glu	AAT Asn	GAG Leu	CTT Leu	GAA Glu	GGC Gly	AGG Arg	CAC His	ATT Ile	TAC Tyr	ATC Ile	TAT Tyr	GTG Val	567
				110					115						120	
CCA Pro	GAC Asp	CCA Pro	GAT Asp	GTA Val	GCC Ala	TTT Phe	GTA Val	CCT Pro	CTA Leu	GGA Gly	ATG Met	ACG Thr	GAT Asp	TAT Tyr	TTA Leu	615
			125					130					135			
GTC Val	ATC Ile	GTG Val	GAG Glu	GAT Asp	GAT Asp	GAT Asp	TCT Ser	GCC Ala	ATT Ile	ATA Ile	CCT Pro	TGT Cys	CGC Arg	ACA Thr	ACT Thr	663
		140					145					150				
GAT Asp	CCC Pro	GAG Glu	ACT Thr	CCT Pro	GTA Val	ACC Thr	TTA Leu	CAC His	AAC Asn	AGT Ser	GAG Glu	GGG Gly	GTG Val	GTA Val	CCT Pro	711
	155					160					165					
GCC Ala	TCC Ser	TAC Tyr	GAC Asp	AGC Ser	AGA Arg	CAG Gln	GGC Gly	TTT Phe	AAT Asn	GGG Gly	ACC Thr	TTC Phe	ACT Thr	GTA Val	GGG Gly	759
	170				175				180						185	
CCC Pro	TAT Tyr	ATC Ile	TGT Cys	GAG Glu	GCC Ala	ACC Thr	GTC Val	AAA Lys	GGA Gly	AAG Lys	AAG Lys	TTC Phe	CAG Gln	ACC Thr	ATC Ile	807
				190				195					200			
CCA Pro	TTT Phe	AAT Asn	GTT Val	TAT Tyr	GCT Ala	TTA Leu	AAA Lys	GCA Ala	ACA Thr	TCA Ser	GAG Glu	CTG Leu	GAT Asp	CTA Leu	GAA Glu	855
			205				210						215			
ATG Met	GAA Glu	GCT Ala	CTT Leu	AAA Lys	ACC Thr	GTG Val	TAT Tyr	AAG Lys	TCA Ser	GGG Gly	GAA Glu	ACG Thr	ATT Ile	GTG Val	GTC Val	903
	220					225						230				
ACC Thr	TGT Cys	GCT Ala	GTT Val	TTT Phe	AAC Asn	AAT Asn	GAG Glu	GTG Val	GTT Val	GAC Asp	CTT Leu	CAA Gln	TGG Trp	ACT Thr	TAC Tyr	951
	235					240					245					
CCT Pro	GGA Gly	GAA Glu	GTG Val	AAA Lys	GGC Gly	AAA Lys	GGC Gly	ATC Ile	ACA Thr	ATA Ile	CTG Leu	GAA Glu	GAA Glu	ATC Ile	AAA Lys	999
	250				255			260							265	
GTC Val	CCA Pro	TCC Ser	ATC Ile	AAA Lys	TTG Leu	GTG Val	TAC Tyr	ACT Thr	TTG Leu	ACG Thr	GTC Val	CCC Pro	GAG Glu	GCC Ala	ACG Thr	1047
				270				275							280	

GTG AAA GAC AGT GGA GAT TAC GAA TGT GCT GCC CGC CAG GCT ACC AGG Val Lys Asp Ser Gly Asp Tyr Glu Cys Ala Ala Arg Gln Ala Thr Arg 285 290 295	1095
GAG GTC AAA GAA ATG AAG AAA GTC ACT ATT TCT GTC CAT GAG AAA GGT Glu Val Lys Glu Met Lys Lys Val Thr Ile Ser Val His Glu Lys Gly 300 305 310	1143
TTC ATT GAA ATC AAA CCC ACC TTC AGC CAG TTG GAA GCT GTC AAC CTG Phe Ile Glu Ile Lys Pro Thr Phe Ser Gln Leu Ala Val Asn Leu 315 320 325	1191
CAT GAA GTC AAA CAT TTT GTT GTA GAG GTG CGG GCC TAC CCA CCT CCC His Glu Val Lys His Phe Val Val Glu Val Arg Ala Tyr Pro Pro Pro 330 335 340 345	1239
AGG ATA TCC TGG CTG AAA AAC AAT CTG ACT CTG ATT GAA AAT CTC ACT Arg Ile Ser Trp Leu Lys Asn Asn Leu Thr Leu Ile Glu Asn Leu Thr 350 355 360	1287
GAG ATC ACC ACT GAT GTG GAA AAG ATT CAG GAA ATA AGG TAT CGA AGC Glu Ile Thr Thr Asp Val Glu Lys Ile Gln Glu Ile Arg Tyr Arg Ser 365 370 375	1335
AAA TTA AAG CTG ATC CGT GCT AAG GAA GAA GAC AGT GGC CAT TAT ACT Lys Leu Lys Leu Ile Arg Ala Lys Glu Glu Asp Ser Gly His Tyr Thr 380 385 390	1383
ATT GTA GCT CAA AAT GAA GAT GCT GTG AAG AGC TAT ACT TTT GAA CTG Ile Val Ala Gln Asn Glu Asp Ala Val Lys Ser Tyr Thr Phe Glu Leu 395 400 405	1431
TTA ACT CAA GTT CCT TCA TCC ATT CTG GAC TTG GTC GAT GAT CAC CAT Leu Thr Gln Val Pro Ser Ser Ile Leu Asp Leu Val Asp Asp His His 410 415 420 425	1479
GGC TCA ACT GGG GGA CAG ACG GTG AGG TGC ACA GCT GAA GGC ACG CCG Gly Ser Thr Gly Gly Gln Thr Val Arg Cys Thr Ala Glu Gly Thr Pro 430 435 440	1527
CTT CCT GAT ATT GAG TGG ATG ATA TGC AAA GAT ATT AAG AAA TGT AAT Leu Pro Asp Ile Glu Trp Met Ile Cys Lys Asp Ile Lys Lys Cys Asn 445 450 455	1575
AAT GAA ACT TCC TGG ACT ATT TTG GCC AAC AAT GTC TCA AAC ATC ATC Asn Glu Thr Ser Trp Thr Ile Leu Ala Asn Asn Val Ser Asn Ile Ile 460 465 470	1623
ACG GAG ATC CAC TCC CGA GAC AGG AGT ACC GTG GAG GGC CGT GTG ACT Thr Glu Ile His Ser Arg Asp Arg Ser Thr Val Glu Gly Arg Val Thr 475 480 485	1671

TTC	GCC	AAA	GTG	GAG	GAG	ACC	ATC	GCC	GTG	CGA	TGC	CTG	GCT	AAG	AAT	1719
Phe	Ala	Lys	Val	Glu	Glu	Thr	Ile	Ala	Val	Arg	Cys	Leu	Ala	Lys	Asn	
490				495					500					505		
CTC	CTT	GGA	GCT	GAG	AAC	CGA	GAG	CTG	AAG	CTG	GTG	GCT	CCC	ACC	CTG	1767
Leu	Leu	Gly	Ala	Glu	Asn	Arg	Glu	Leu	Lys	Leu	Val	Ala	Pro	Thr	Leu	
				510				515						520		
CGT	TCT	GAA	CTC	ACG	GTG	GCT	GCT	GCA	GTG	CTG	GTG	CTG	TTG	GTG	ATT	1815
Arg	Ser	Glu	Leu	Thr	Val	Ala	Ala	Ala	Val	Leu	Val	Leu	Leu	Val	Ile	
			525					530					535			
GTG	ATC	ATC	TCA	CTT	ATT	GTC	CTG	GTT	GTC	ATT	TGG	AAA	CAG	AAA	CCG	1863
Val	Ile	Ile	Ser	Leu	Ile	Val	Leu	Val	Val	Ile	Trp	Lys	Gln	Lys	Pro	
			540				545					550				
AGG	TAT	GAA	ATT	CGC	TGG	AGG	GTC	ATT	GAA	TCA	ATC	AGC	CCG	GAT	GGA	1911
Arg	Tyr	Glu	Ile	Arg	Trp	Arg	Val	Ile	Glu	Ser	Ile	Ser	Pro	Asp	Gly	
			555				560				565					
CAT	GAA	TAT	ATT	TAT	GTG	GAC	CCG	ATG	CAG	CTG	CCT	TAT	GAC	TCA	AGA	1959
His	Glu	Tyr	Ile	Tyr	Val	Asp	Pro	Met	Gln	Leu	Pro	Tyr	Asp	Ser	Arg	
					575					580					585	
TGG	GAG	TTT	CCA	AGA	GAT	GGA	CTA	GTG	CTT	GGT	CGG	GTC	TTG	GGG	TCT	2007
Trp	Glu	Phe	Pro	Arg	Asp	Gly	Leu	Val	Leu	Gly	Arg	Val	Leu	Gly	Ser	
				590					595					600		
GGA	GCG	TTT	GGG	AAG	GTG	GTT	GAA	GGA	ACA	GCC	TAT	GGA	TTA	AGC	CGG	2055
Gly	Ala	Phe	Gly	Lys	Val	Val	Glu	Gly	Thr	Ala	Tyr	Gly	Leu	Ser	Arg	
			605					610					615			
TCC	CAA	CCT	GTC	ATG	AAA	GTT	GCA	GTG	AAG	ATG	CTA	AAA	CCC	ACG	GCC	2103
Ser	Gln	Pro	Val	Met	Lys	Val	Ala	Val	Lys	Met	Leu	Lys	Pro	Thr	Ala	
			620				625						630			
AGA	TCC	AGT	GAA	AAA	CAA	GCT	CTC	ATG	TCT	GAA	CTG	AAG	ATA	ATG	ACT	2151
Arg	Ser	Ser	Glu	Lys	Gln	Ala	Leu	Met	Ser	Glu	Leu	Lys	Ile	Met	Thr	
			635				640					645				
CAC	CTG	GGG	CCA	CAT	TTG	AAC	ATT	GTA	AAC	TTG	CTG	GGA	GCC	TGC	ACC	2199
His	Leu	Gly	Pro	His	Leu	Asn	Ile	Val	Asn	Leu	Leu	Gly	Ala	Cys	Thr	
					655					660				665		
AAG	TCA	GGC	CCC	ATT	TAC	ATC	ATC	ACA	GAG	TAT	TGC	TTC	TAT	GGA	GAT	2247
Lys	Ser	Gly	Pro	Ile	Tyr	Ile	Ile	Thr	Glu	Tyr	Cys	Phe	Tyr	Gly	Asp	
				670					675					680		
TTG	GTC	AAC	TAT	TTG	CAT	AAG	AAT	AGG	GAT	AGC	TTC	CTG	AGC	CAC	CAC	2295
Leu	Val	Asn	Tyr	Leu	His	Lys	Asn	Arg	Asp	Ser	Phe	Leu	Ser	His	His	
				685				690					695			
CCA	GAG	AAG	CCA	AAG	AAA	GAG	CTG	GAT	ATC	TTT	GGA	TTG	AAC	CCT	GCT	2343
Pro	Glu	Lys	Pro	Lys	Lys	Glu	Leu	Asp	Ile	Phe	Gly	Leu	Asn	Pro	Ala	
			700				705						710			

GAT Asp	GAA Glu	AGC Ser	ACA Thr	CGG Arg	AGC Ser	TAT Tyr	GTT Val	ATT Ile	TTA Leu	TCT Ser	TTT Phe	GAA Glu	AAC Asn	AAT Asn	GGT Gly	2391
715						720					725					
GAC Asp	TAC Tyr	ATG Met	GAC Asp	ATG Met	AAG Lys	CAG Gln	GCT Ala	GAT Asp	ACT Thr	ACA Thr	CAG Gln	TAT Tyr	GTC Val	CCC Pro	ATG Met	2439
730					735					740					745	
CTA Leu	GAA Glu	AGG Arg	AAA Lys	GAG Glu	GTT Val	TCT Ser	AAA Lys	TAT Tyr	TCC Ser	GAC Asp	ATC Ile	CAG Gln	AGA Arg	TCA Ser	CTC Leu	2487
				750					755						760	
TAT Tyr	GAT Asp	CGT Arg	CCA Pro	GCC Ala	TCA Ser	TAT Tyr	AAG Lys	AAG Lys	AAA Lys	TCT Ser	ATG Met	TTA Leu	GAC Asp	TCA Ser	GAA Glu	2535
			765					770					775			
GTC Val	AAA Lys	AAC Asn	CTC Leu	CTT Leu	TCA Ser	GAT Asp	GAT Asp	AAC Asn	TCA Ser	GAA Glu	GGC Gly	CTT Leu	ACT Thr	TTA Leu	TTG Leu	2583
		780					785					790				
GAT Asp	TTG Leu	TTG Leu	AGC Ser	TTC Phe	ACC Thr	TAT Tyr	CAA Gln	GTT Val	GCC Ala	CGA Arg	GGA Gly	ATG Met	GAG Glu	TTT Phe	TTG Leu	2631
	795					800					805					
GCT Ala	TCA Ser	AAA Lys	AAT Asn	TGT Cys	GTC Val	CAC His	CGT Arg	GAT Asp	CTG Leu	GCT Ala	GCT Ala	CGC Arg	AAC Asn	GTC Val	CTC Leu	2679
810					815					820					825	
CTG Leu	GCA Ala	CAA Gln	GGA Gly	AAA Lys	ATT Ile	GTG Val	AAG Lys	ATC Ile	TGT Cys	GAC Asp	TTT Phe	GGC Gly	CTG Leu	GCC Ala	AGA Arg	2727
				830					835					840		
GAC Asp	ATC Ile	ATG Met	CAT His	GAT Asp	TCG Ser	AAC Asn	TAT Tyr	GTG Val	TCG Ser	AAA Lys	GGC Gly	AGT Ser	ACC Thr	TTT Phe	CTG Leu	2775
			845					850					855			
CCC Pro	GTG Val	AAG Lys	TGG Trp	ATG Met	GCT Ala	CCT Pro	GAG Glu	AGC Ser	ATC Ile	TTT Phe	GAC Asp	AAC Asn	CTC Leu	TAC Tyr	ACC Thr	2823
		860					865					870				
ACA Thr	CTG Leu	AGT Ser	GAT Asp	GTC Val	TGG Trp	TCT Ser	TAT Tyr	GGC Gly	ATT Ile	CTG Leu	CTC Leu	TGG Trp	GAG Glu	ATC Ile	TTT Phe	2871
	875					880					885					
TCC Ser	CTT Leu	GGT Gly	GGC Gly	ACC Thr	CCT Pro	TAC Tyr	CCC Pro	GGC Gly	ATG Met	ATG Met	GTG Val	GAT Asp	TCT Ser	ACT Thr	TTC Phe	2919
890					895					900					905	
TAC Tyr	AAT Asn	AAG Lys	ATC Ile	AAG Lys	AGT Ser	GGG Gly	TAC Tyr	CGG Arg	ATG Met	GCC Ala	AAG Lys	CCT Pro	GAC Asp	CAC His	GCT Ala	2967
				910					915						920	

ACC AGT GAA GTC TAC GAG ATC ATG GTG AAA TGC TGG AAC AGT GAG CCG Thr Ser Glu Val Tyr Glu Ile Met Val Lys Cys Trp Asn Ser Glu Pro	3015
925 930 935	
GAG AAG AGA CCC TCC TTT TAC CAC CTG AGT GAG ATT GTG GAG AAT CTG Glu Lys Arg Pro Ser Phe Tyr His Leu Ser Glu Ile Val Glu Asn Leu	3063
940 945 950	
CTG CCT GGA CAA TAT AAA AAG AGT TAT GAA AAA ATT CAC CTG GAC TTC Leu Pro Gly Gln Tyr Lys Lys Ser Tyr Glu Lys Ile His Leu Asp Phe	3111
955 960 965	
CTG AAG AGT GAC CAT CCT GCT GTG GCA CGC ATG CGT GTG GAC TCA GAC Leu Lys Ser Asp His Pro Ala Val Ala Arg Met Arg Val Asp Ser Asp	3159
970 975 980 985	
AAT GCA TAC ATT GGT GTC ACC TAC AAA AAC GAG GAA GAC AAG CTG AAG Asn Ala Tyr Ile Gly Val Thr Tyr Lys Asn Glu Glu Asp Lys Leu Lys	3207
990 995 1000	
GAC TGG GAG GGT GGT CTG GAT GAG CAG AGA CTG AGC GCT GAC AGT GGC Asp Trp Glu Gly Gly Leu Asp Glu Gln Arg Leu Ser Ala Asp Ser Gly	3255
1005 1010 1015	
TAC ATC ATT CCT CTG CCT GAC ATT GAC CCT GTC CCT GAG GAG GAG GAC Tyr Ile Ile Pro Leu Pro Asp Ile Asp Pro Val Pro Glu Glu Glu Asp	3303
1020 1025 1030	
CTG GGC AAG AGG AAC AGA CAC AGC TCG CAG ACC TCT GAA GAG AGT GCC Leu Gly Lys Arg Asn Arg His Ser Ser Gln Thr Ser Glu Glu Ser Ala	3351
1035 1040 1045	
ATT GAG ACG GGT TCC AGC AGT TCC ACC TTC ATC AAG AGA GAG GAC GAG Ile Glu Thr Gly Ser Ser Ser Thr Phe Ile Lys Arg Glu Asp Glu	3399
1050 1055 1060 1065	
ACC ATT GAA GAC ATC GAC ATG ATG GAC GAC ATC GGC ATA GAC TCT TCA Thr Ile Glu Asp Ile Asp Met Met Asp Asp Ile Gly Ile Asp Ser Ser	3447
1070 1075 1080	
GAC CTG GTG GAA GAC AGC TTC CTG TAACTGGCGG ATTCGAGGGG TTCCTCCAC Asp Leu Val Glu Asp Ser Phe Leu	3501
1085	
TTCTGGGGCC ACCTCTGGAT CCCGTTTCTGAA AAACCACTTT ATTGCAATGC GGAGGTTGAG	3561
AGGAGGACTT GGTGATGTT TAAAGAGAAG TTCCAGCCA AGGGCCTCGG GGAGCGTTCT	3621
AAATATGAAT GAATGGGATA TTTTGAAATG AACTTTGTCA GTGTTGCCTC TTGCAATGCC	3681
TCAGTAGCAT CTCAGTGGTG TGTAAGTTT GGAGATAGAT GGATAAGGGA ATAATAGGCC	3741
ACAGAAGGTG AACTTTGTGC TTCAAGGACA TTGGTGAGAG TCCAACAGAC ACAATTTATA	3801
CTGCGACAGA ACTTCAGCAT TGTAATTATG TAAATAACTC TAACCAAGGC TGTGTTTGA	3861

TTGTATTAAC TATCTTCTTT GGACTTCTGA AGAGACCACT CAATCCATCC TGTACTTCCC 3921
TCTTGAAACC TGATGTAGCT GCTGTTGAAC TTTTAAAGA AGTGCATGAA AAACCATTTT 3981
TGAACCTTAA AAGGTACTGG TACTATAGCA TTTTGCTATC TTTTITAGTG TTAAAGAGAT 4041
AAAGAATAAT AAG 4054

(2) INFORMATION FOR SEQ ID NO:36:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1089 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Gly Thr Ser His Pro Ala Phe Leu Val Leu Gly Cys Leu Leu Thr
1 5 10 15
Gly Leu Ser Leu Ile Leu Cys Gln Leu Ser Leu Pro Ser Ile Leu Pro
20 25 30
Asn Glu Asn Glu Lys Val Val Gln Leu Asn Ser Ser Phe Ser Leu Arg
35 40 45
Cys Phe Gly Glu Ser Glu Val Ser Trp Gln Tyr Pro Met Ser Glu Glu
50 55 60
Glu Ser Ser Asp Val Glu Ile Arg Asn Glu Glu Asn Asn Ser Gly Leu
65 70 75 80
Phe Val Thr Val Leu Glu Val Ser Ser Ala Ser Ala Ala His Thr Gly
85 90 95
Leu Tyr Thr Cys Tyr Tyr Asn His Thr Gln Thr Glu Glu Asn Glu Leu
100 105 110
Glu Gly Arg His Ile Tyr Ile Tyr Val Pro Asp Pro Asp Val Ala Phe
115 120 125
Val Pro Leu Gly Met Thr Asp Tyr Leu Val Ile Val Glu Asp Asp Asp
130 135 140
Ser Ala Ile Ile Pro Cys Arg Thr Thr Asp Pro Glu Thr Pro Val Thr
145 150 155 160
Leu His Asn Ser Glu Gly Val Val Pro Ala Ser Tyr Asp Ser Arg Gln
165 170 175

Gly Phe Asn Gly Thr Phe Thr Val Gly Pro Tyr Ile Cys Glu Ala Thr
 180 185 190
 Val Lys Gly Lys Lys Phe Gln Thr Ile Pro Phe Asn Val Tyr Ala Leu
 195 200 205
 Lys Ala Thr Ser Glu Leu Asp Leu Glu Met Glu Ala Leu Lys Thr Val
 210 215 220
 Tyr Lys Ser Gly Glu Thr Ile Val Val Thr Cys Ala Val Phe Asn Asn
 225 230 235 240
 Glu Val Val Asp Leu Gln Trp Thr Tyr Pro Gly Glu Val Lys Gly Lys
 245 250 255
 Gly Ile Thr Ile Leu Glu Glu Ile Lys Val Pro Ser Ile Lys Leu Val
 260 265 270
 Tyr Thr Leu Thr Val Pro Glu Ala Thr Val Lys Asp Ser Gly Asp Tyr
 275 280 285
 Glu Cys Ala Ala Arg Gln Ala Thr Arg Glu Val Lys Glu Met Lys Lys
 290 295 300
 Val Thr Ile Ser Val His Glu Lys Gly Phe Ile Glu Ile Lys Pro Thr
 305 310 315 320
 Phe Ser Gln Leu Glu Ala Val Asn Leu His Glu Val Lys His Phe Val
 325 330 335
 Val Glu Val Arg Ala Tyr Pro Pro Pro Arg Ile Ser Trp Leu Lys Asn
 340 345 350
 Asn Leu Thr Leu Ile Glu Asn Leu Thr Glu Ile Thr Thr Asp Val Glu
 355 360 365
 Lys Ile Gln Glu Ile Arg Tyr Arg Ser Lys Leu Lys Leu Ile Arg Ala
 370 375 380
 Lys Glu Glu Asp Ser Gly His Tyr Thr Ile Val Ala Gln Asn Glu Asp
 385 390 395 400
 Ala Val Lys Ser Tyr Thr Phe Glu Leu Leu Thr Gln Val Pro Ser Ser
 405 410 415
 Ile Leu Asp Leu Val Asp Asp His His Gly Ser Thr Gly Gly Gln Thr
 420 425 430
 Val Arg Cys Thr Ala Glu Gly Thr Pro Leu Pro Asp Ile Glu Trp Met
 435 440 445
 Ile Cys Lys Asp Ile Lys Lys Cys Asn Asn Glu Thr Ser Trp Thr Ile
 450 455 460

Leu Ala Asn Asn Val Ser Asn Ile Ile Thr Glu Ile His Ser Arg Asp
 465 470 475 480
 Arg Ser Thr Val Glu Gly Arg Val Thr Phe Ala Lys Val Glu Glu Thr
 485 490 495
 Ile Ala Val Arg Cys Leu Ala Lys Asn Leu Leu Gly Ala Glu Asn Arg
 500 505 510
 Glu Leu Lys Leu Val Ala Pro Thr Leu Arg Ser Glu Leu Thr Val Ala
 515 520 525
 Ala Ala Val Leu Val Leu Leu Val Ile Val Ile Ile Ser Leu Ile Val
 530 535 540
 Leu Val Val Ile Trp Lys Gln Lys Pro Arg Tyr Glu Ile Arg Trp Arg
 545 550 555 560
 Val Ile Glu Ser Ile Ser Pro Asp Gly His Glu Tyr Ile Tyr Val Asp
 565 570 575
 Pro Met Gln Leu Pro Tyr Asp Ser Arg Trp Glu Phe Pro Arg Asp Gly
 580 585 590
 Leu Val Leu Gly Arg Val Leu Gly Ser Gly Ala Phe Gly Lys Val Val
 595 600 605
 Glu Gly Thr Ala Tyr Gly Leu Ser Arg Ser Gln Pro Val Met Lys Val
 610 615 620
 Ala Val Lys Met Leu Lys Pro Thr Ala Arg Ser Ser Glu Lys Gln Ala
 625 630 635 640
 Leu Met Ser Glu Leu Lys Ile Met Thr His Leu Gly Pro His Leu Asn
 645 650 655
 Ile Val Asn Leu Leu Gly Ala Cys Thr Lys Ser Gly Pro Ile Tyr Ile
 660 665 670
 Ile Thr Glu Tyr Cys Phe Tyr Gly Asp Leu Val Asn Tyr Leu His Lys
 675 680 685
 Asn Arg Asp Ser Phe Leu Ser His His Pro Glu Lys Pro Lys Lys Glu
 690 695 700
 Leu Asp Ile Phe Gly Leu Asn Pro Ala Asp Glu Ser Thr Arg Ser Tyr
 705 710 715 720
 Val Ile Leu Ser Phe Glu Asn Asn Gly Asp Tyr Met Asp Met Lys Gln
 725 730 735
 Ala Asp Thr Thr Gln Tyr Val Pro Met Leu Glu Arg Lys Glu Val Ser
 740 745 750

135

Ser Ser Gln Thr Ser Glu Glu Ser Ala Ile Glu Thr Gly Ser Ser Ser
 1045 1050 1055

Ser Thr Phe Ile Lys Arg Glu Asp Glu Thr Ile Glu Asp Ile Asp Met
 1060 1065 1070

Met Asp Asp Ile Gly Ile Asp Ser Ser Asp Leu Val Glu Asp Ser Phe
 1075 1080 1085

Leu

00400500
 159311

137